



1648

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/855,754A

DATE: 06/06/2002

TIME: 12:32:52

Input Set : A:\03495206.txt

Output Set: N:\CRF3\06062002\I855754A.raw

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: BOURSAUX-EUDE, CAROLINE
4 GUIZO-MACLOUF, NICOLE
6 <120> TITLE OF INVENTION: POLYPEPTIDES CONTAINING POLYMORPHISMS OF THE REPEATED
7 REGIONS OF PERTACTIN IN BORDETELLA PERTUSSIS,
8 BORDETELLA PARAPERTUSSIS, AND BORDETELLA
9 BRONCHISEPTICA, THEIR USE IN DIAGNOSTICS, AND IN
10 IMMUNOGENIC COMPOSITIONS
12 <130> FILE REFERENCE: 03495-0206-00000
14 <140> CURRENT APPLICATION NUMBER: 09/855,754A
15 <141> CURRENT FILING DATE: 2000-11-15
17 <150> PRIOR APPLICATION NUMBER: 60/206,969
18 <151> PRIOR FILING DATE: 2000-05-25
E--> 20 <160> NUMBER OF SEQ ID NOS: 24 25
22 <170> SOFTWARE: PatentIn Ver. 2.1

see p. 2

ERRORED SEQUENCES

09/855,754A 2

<210> 25 *last sequence in submitted file*

<211> 5

<212> PRT

<213> Artificial *see item 11 on Ena summary sheet*

<220>

<221> MISC_FEATURE

<222> (3)..(4)

<223> Xaa can be any amino acid

<400> 25

Gly Gly Xaa Xaa Pro

1

5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/855,754A

DATE: 06/06/2002

TIME: 12:32:54

Input Set : A:\03495206.txt

Output Set: N:\CRF3\06062002\I855754A.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1065 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (24) Counted (25)

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/855,754A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>
Sequence(s) 25 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.